



## SEQUENCE LISTING

<110> Vanderbilt University  
Balser, Jeffrey  
George, Alfred  
Roden, Dan

<120> HUMAN KCR1 REGULATION OF HERG POTASSIUM CHANNEL BLOCK

<130> 1242-49-2

<140> US/10/000,151

<141> 2001-10-30

<150> 60/244,340

<151> 2000-10-30

<160> 7

<170> PatentIn version 3.0

<210> 1

<211> 1857

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1422)

<223> n is any nucleotide

<400> 1

atg gcg cag cta gag ggt tac tgt ttc tcg gcc gcc ttg agc tgt acc  
48

Met Ala Gln Leu Glu Gly Tyr Cys Phe Ser Ala Ala Leu Ser Cys Thr

1

5

10

15

ttt tta gtg tcc tgc ctc ctc ttc tcc gcc ttc agc cgg gcg ctg cga  
96

Phe Leu Val Ser Cys Leu Leu Phe Ser Ala Phe Ser Arg Ala Leu Arg

20

25

30

gag ccc tac atg gac gag atc ttc cac ctg cct cag gcg cag cgc tac

144  
 Glu Pro Tyr Met Asp Glu Ile Phe His Leu Pro Gln Ala Gln Arg Tyr  
 35 40 45  
 tgt gag ggc cat ttc tcc ctt tcc cag tgg gat ccc atg att act aca  
 192  
 Cys Glu Gly His Phe Ser Leu Ser Gln Trp Asp Pro Met Ile Thr Thr  
 50 55 60  
 tta cct ggc ttg tac ctg gtg tca gtt gga gtg gtc aaa cct gcc att  
 240  
 Leu Pro Gly Leu Tyr Leu Val Ser Val Gly Val Val Lys Pro Ala Ile  
 65 70 75 80  
 tgg atc ttt gga tgg tct gaa cat gtt gtc tgc tcc att ggg atg ctc  
 288  
 Trp Ile Phe Gly Trp Ser Glu His Val Val Cys Ser Ile Gly Met Leu  
 85 90 95  
 aga ttt gtt aat ctt ctc ttc agt gtt ggc aac ttc tat tta cta tat  
 336  
 Arg Phe Val Asn Leu Leu Phe Ser Val Gly Asn Phe Tyr Leu Leu Tyr  
 100 105 110  
 ttg ctt ttc cac aag gta caa ccc aga aac aag gct gcc tca agt atc  
 384  
 Leu Leu Phe His Lys Val Gln Pro Arg Asn Lys Ala Ala Ser Ser Ile  
 115 120 125  
 cag aga gtc ttg tca aca tta aca cta gca gta ttt cca aca ctt tat  
 432  
 Gln Arg Val Leu Ser Thr Leu Thr Leu Ala Val Phe Pro Thr Leu Tyr  
 130 135 140

ttt ttt aac ttc ctt tat tat aca gaa gca gga tct atg ttt ttt act  
480

Phe Phe Asn Phe Leu Tyr Tyr Thr Glu Ala Gly Ser Met Phe Phe Thr

145

150

155

160

ctt ttt gca tat ttg atg tgt ctt tat gga aat cat aaa act tca gcc  
528

Leu Phe Ala Tyr Leu Met Cys Leu Tyr Gly Asn His Lys Thr Ser Ala

165

170

175

ttc ctt gga ttt tgt ggc ttc atg ttt cgg caa aca aat atc atc tgg  
576

Phe Leu Gly Phe Cys Gly Phe Met Phe Arg Gln Thr Asn Ile Ile Trp

180

185

190

gct gtc ttc tgt gca ggg aat gtc att gca caa aag tta act gag gct  
624

Ala Val Phe Cys Ala Gly Asn Val Ile Ala Gln Lys Leu Thr Glu Ala

195

200

205

tgg aaa act gag cta caa aag aag gaa gac aga ctt cca cct att aaa  
672

Trp Lys Thr Glu Leu Gln Lys Lys Glu Asp Arg Leu Pro Pro Ile Lys

210

215

220

gga cca ttt gca gaa ttc aga aaa att ctt cag ttt ctt ttg gct tat  
720

Gly Pro Phe Ala Glu Phe Arg Lys Ile Leu Gln Phe Leu Leu Ala Tyr

225

230

235

240

tcc atg tcc ttt aaa aac ttg agt atg ctt ttc tgt ttg act tgg ccc  
768

Ser Met Ser Phe Lys Asn Leu Ser Met Leu Phe Cys Leu Thr Trp Pro

245

250

255

tac atc ctt ctg gga ttt ctg ttt tgt gct ttt gta gta gtt aat ggt  
816

Tyr Ile Leu Leu Gly Phe Leu Phe Cys Ala Phe Val Val Val Asn Gly

260

265

270

gga att gtt att ggc gat cgg agt agt cat gaa gcc tgt ctt cat ttt  
864

Gly Ile Val Ile Gly Asp Arg Ser Ser His Glu Ala Cys Leu His Phe

275

280

285

cct caa cta ttc tac ttt ttt tca ttt act ctc ttt ttt tct ttt cct  
912

Pro Gln Leu Phe Tyr Phe Phe Ser Phe Thr Leu Phe Phe Ser Phe Pro

290

295

300

cat ctc ctg tct cct agc aaa att aag act ttt ctt tcc tta gtt tgg  
960

His Leu Leu Ser Pro Ser Lys Ile Lys Thr Phe Leu Ser Leu Val Trp

305

310

315

320

aaa cat gga att ctg ttt ttg gtg gtt acc tta gtc tct gtg ttt tta  
1008

Lys His Gly Ile Leu Phe Leu Val Val Thr Leu Val Ser Val Phe Leu

325

330

335

gtt tgg aaa ttc act tat gct cat aaa tac ttg cta gca gac aat aga  
1056

Val Trp Lys Phe Thr Tyr Ala His Lys Tyr Leu Leu Ala Asp Asn Arg

340

345

350

cat tat act ttc tat gtg tgg aaa aga gtt ttt caa aga tat gca att  
1104

His Tyr Thr Phe Tyr Val Trp Lys Arg Val Phe Gln Arg Tyr Ala Ile

355

360

365

ctg aaa tat ttg tta gtt cca gcc tat ata ttt gct ggt tgg agt ata  
1152

Leu Lys Tyr Leu Leu Val Pro Ala Tyr Ile Phe Ala Gly Trp Ser Ile

370

375

380

gct gac tca ttg aaa tca aag cca att ttt tgg aat tta atg ttt ttc  
1200

Ala Asp Ser Leu Lys Ser Lys Pro Ile Phe Trp Asn Leu Met Phe Phe

385

390

395

400

ata tgc ttg ttc att gtt ata gtt cct cag aaa ctg ctg gaa ttt cgt  
1248

Ile Cys Leu Phe Ile Val Ile Val Pro Gln Lys Leu Leu Glu Phe Arg

405

410

415

tac ttc att tta cct tat gtc att tat agg ctt aac ata act ctg cct  
1296

Tyr Phe Ile Leu Pro Tyr Val Ile Tyr Arg Leu Asn Ile Thr Leu Pro

420

425

430

ccc aca tcc aga ctt gtt tgt gaa ctg agt tgc tat gca att gtt aat  
1344

Pro Thr Ser Arg Leu Val Cys Glu Leu Ser Cys Tyr Ala Ile Val Asn

435

440

445

ttc ata act ttt tac atc ttt ctg aac aag act ttt cag tgg cca aat  
1392

Phe Ile Thr Phe Tyr Ile Phe Leu Asn Lys Thr Phe Gln Trp Pro Asn

450

455

460

agt cag gac att caa agg ttt atg tgg taa tatcagtgat attttgaact  
1442

Ser Gln Asp Ile Gln Arg Phe Met Trp

465

470

gtaaaaatgg acttaataat agaccatttc tacaaagaac aactgaatag gnggaaaaca  
1502

tggaatttct tttaggtgca gtggtggtct tcaaattaca ttagtttttt taatatatat  
1562

tttaaacata tgtaagaaat taagtggcaa agaactggga aagcttaaga cctgcttcaa  
1622

angcctgaat aatgggaaaa taaanwngtt tncagatatc tcatatcgct cnnknatgn  
1682

tggcccytmn caangcttgg gaatgkttnn wntgnataag ttnattaaan ctgggnntgc  
1742

tnnmwatnac ttnnkncca nccwnnnwac natgnnntan nnantattta caaaggtcag  
1802

gtgatattct tgactgaaaa gtgctctnaa cataaaagta aatatnggcc ncaaa  
1857

<210> 2

<211> 473

<212> PRT

<213> Homo sapiens

<400> 2

Met	Ala	Gln	Leu	Glu	Gly	Tyr	Cys	Phe	Ser	Ala	Ala	Leu	Ser	Cys	Thr
1				5					10					15	

Phe	Leu	Val	Ser	Cys	Leu	Leu	Phe	Ser	Ala	Phe	Ser	Arg	Ala	Leu	Arg
			20					25					30		

Glu	Pro	Tyr	Met	Asp	Glu	Ile	Phe	His	Leu	Pro	Gln	Ala	Gln	Arg	Tyr
		35					40					45			

Cys	Glu	Gly	His	Phe	Ser	Leu	Ser	Gln	Trp	Asp	Pro	Met	Ile	Thr	Thr
	50						55					60			

Leu Pro Gly Leu Tyr Leu Val Ser Val Gly Val Val Lys Pro Ala Ile  
65 70 75 80

Trp Ile Phe Gly Trp Ser Glu His Val Val Cys Ser Ile Gly Met Leu  
85 90 95

Arg Phe Val Asn Leu Leu Phe Ser Val Gly Asn Phe Tyr Leu Leu Tyr  
100 105 110

Leu Leu Phe His Lys Val Gln Pro Arg Asn Lys Ala Ala Ser Ser Ile  
115 120 125

Gln Arg Val Leu Ser Thr Leu Thr Leu Ala Val Phe Pro Thr Leu Tyr  
130 135 140

Phe Phe Asn Phe Leu Tyr Tyr Thr Glu Ala Gly Ser Met Phe Phe Thr  
145 150 155 160

Leu Phe Ala Tyr Leu Met Cys Leu Tyr Gly Asn His Lys Thr Ser Ala  
165 170 175

Phe Leu Gly Phe Cys Gly Phe Met Phe Arg Gln Thr Asn Ile Ile Trp  
180 185 190

Ala Val Phe Cys Ala Gly Asn Val Ile Ala Gln Lys Leu Thr Glu Ala  
195 200 205

Trp Lys Thr Glu Leu Gln Lys Lys Glu Asp Arg Leu Pro Pro Ile Lys  
210 215 220

Gly Pro Phe Ala Glu Phe Arg Lys Ile Leu Gln Phe Leu Leu Ala Tyr  
225 230 235 240

Ser Met Ser Phe Lys Asn Leu Ser Met Leu Phe Cys Leu Thr Trp Pro  
245 250 255

Tyr Ile Leu Leu Gly Phe Leu Phe Cys Ala Phe Val Val Val Asn Gly  
                   260                  265                  270

Gly Ile Val Ile Gly Asp Arg Ser Ser His Glu Ala Cys Leu His Phe  
                   275                  280                  285

Pro Gln Leu Phe Tyr Phe Phe Ser Phe Thr Leu Phe Phe Ser Phe Pro  
                   290                  295                  300

His Leu Leu Ser Pro Ser Lys Ile Lys Thr Phe Leu Ser Leu Val Trp  
   305                  310                  315                  320

Lys His Gly Ile Leu Phe Leu Val Val Thr Leu Val Ser Val Phe Leu  
                   325                  330                  335

Val Trp Lys Phe Thr Tyr Ala His Lys Tyr Leu Leu Ala Asp Asn Arg  
                   340                  345                  350

His Tyr Thr Phe Tyr Val Trp Lys Arg Val Phe Gln Arg Tyr Ala Ile  
                   355                  360                  365

Leu Lys Tyr Leu Leu Val Pro Ala Tyr Ile Phe Ala Gly Trp Ser Ile  
                   370                  375                  380

Ala Asp Ser Leu Lys Ser Lys Pro Ile Phe Trp Asn Leu Met Phe Phe  
   385                  390                  395                  400

Ile Cys Leu Phe Ile Val Ile Val Pro Gln Lys Leu Leu Glu Phe Arg  
                   405                  410                  415

Tyr Phe Ile Leu Pro Tyr Val Ile Tyr Arg Leu Asn Ile Thr Leu Pro  
                   420                  425                  430

Pro Thr Ser Arg Leu Val Cys Glu Leu Ser Cys Tyr Ala Ile Val Asn  
                   435                  440                  445



Phe Ile Thr Phe Tyr Ile Phe Leu Asn Lys Thr Phe Gln Trp Pro Asn  
 450 455 460

Ser Gln Asp Ile Gln Arg Phe Met Trp  
 465 470

<210> 3  
 <211> 1159  
 <212> PRT  
 <213> Homo sapiens

<400> 3

Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Phe Leu Asp  
 1 5 10 15

Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Ile Ile Ala  
 20 25 30

Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly Phe  
 35 40 45

Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro Cys  
 50 55 60

Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala Ala  
 65 70 75 80

Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu Ile  
 85 90 95

Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp Val  
 100 105 110

Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn  
 115 120 125

Phe Glu Val Val Met Glu Lys Asp Met Val Gly Ser Pro Ala His Asp  
 130 135 140

Thr Asn His Arg Gly Pro Pro Thr Ser Trp Leu Ala Pro Gly Arg Ala  
 145 150 155 160

Lys Thr Phe Arg Leu Lys Leu Pro Ala Leu Leu Ala Leu Thr Ala Arg  
 165 170 175

Glu	Ser	Ser	Val	Arg	Ser	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Ala	Pro	Gly			
			180					185					190					
Ala	Val	Val	Val	Asp	Val	Asp	Leu	Thr	Pro	Ala	Ala	Pro	Ser	Ser	Glu			
			195				200					205						
Ser	Leu	Ala	Leu	Asp	Glu	Val	Thr	Ala	Met	Asp	Asn	His	Val	Ala	Gly			
	210					215					220							
Leu	Gly	Pro	Ala	Glu	Glu	Arg	Arg	Ala	Leu	Val	Gly	Pro	Gly	Ser	Pro			
225					230					235					240			
Pro	Arg	Ser	Ala	Pro	Gly	Gln	Leu	Pro	Ser	Pro	Arg	Ala	His	Ser	Leu			
				245					250					255				
Asn	Pro	Asp	Ala	Ser	Gly	Ser	Ser	Cys	Ser	Leu	Ala	Arg	Thr	Arg	Ser			
			260					265					270					
Arg	Glu	Ser	Cys	Ala	Ser	Val	Arg	Arg	Ala	Ser	Ser	Ala	Asp	Asp	Ile			
		275					280					285						
Glu	Ala	Met	Arg	Ala	Gly	Val	Leu	Pro	Pro	Pro	Pro	Arg	His	Ala	Ser			
	290					295					300							
Thr	Gly	Ala	Met	His	Pro	Leu	Arg	Ser	Gly	Leu	Leu	Asn	Ser	Thr	Ser			
305					310					315					320			
Asp	Ser	Asp	Leu	Val	Arg	Tyr	Arg	Thr	Ile	Ser	Lys	Ile	Pro	Gln	Ile			
				325					330					335				
Thr	Leu	Asn	Phe	Val	Asp	Leu	Lys	Gly	Asp	Pro	Phe	Leu	Ala	Ser	Pro			
			340					345					350					
Thr	Ser	Asp	Arg	Glu	Ile	Ile	Ala	Pro	Lys	Ile	Lys	Glu	Arg	Thr	His			
		355					360					365						
Asn	Val	Thr	Glu	Lys	Val	Thr	Gln	Val	Leu	Ser	Leu	Gly	Ala	Asp	Val			
	370					375					380							
Leu	Pro	Glu	Tyr	Lys	Leu	Gln	Ala	Pro	Arg	Ile	His	Arg	Trp	Thr	Ile			
385					390					395					400			
Leu	His	Tyr	Ser	Pro	Phe	Lys	Ala	Val	Trp	Asp	Trp	Leu	Ile	Leu	Leu			
				405					410					415				
Leu	Val	Ile	Tyr	Thr	Ala	Val	Phe	Thr	Pro	Tyr	Ser	Ala	Ala	Phe	Leu			
			420					425					430					

Leu	Lys	Glu	Thr	Glu	Glu	Gly	Pro	Pro	Ala	Thr	Glu	Cys	Gly	Tyr	Ala		
		435					440					445					
Cys	Gln	Pro	Leu	Ala	Val	Val	Asp	Leu	Ile	Val	Asp	Ile	Met	Phe	Ile		
	450					455					460						
Val	Asp	Ile	Leu	Ile	Asn	Phe	Arg	Thr	Thr	Tyr	Val	Asn	Ala	Asn	Glu		
465					470					475					480		
Glu	Val	Val	Ser	His	Pro	Gly	Arg	Ile	Ala	Val	His	Tyr	Phe	Lys	Gly		
				485					490					495			
Trp	Phe	Leu	Ile	Asp	Met	Val	Ala	Ala	Ile	Pro	Phe	Asp	Leu	Leu	Ile		
			500					505					510				
Phe	Gly	Ser	Gly	Ser	Glu	Glu	Leu	Ile	Gly	Leu	Leu	Lys	Thr	Ala	Arg		
		515					520					525					
Leu	Leu	Arg	Leu	Val	Arg	Val	Ala	Arg	Lys	Leu	Asp	Arg	Tyr	Ser	Glu		
	530					535					540						
Tyr	Gly	Ala	Ala	Val	Leu	Phe	Leu	Leu	Met	Cys	Thr	Phe	Ala	Leu	Ile		
545					550					555					560		
Ala	His	Trp	Leu	Ala	Cys	Ile	Trp	Tyr	Ala	Ile	Gly	Asn	Met	Glu	Gln		
				565					570					575			
Pro	His	Met	Asp	Ser	Arg	Ile	Gly	Trp	Leu	His	Asn	Leu	Gly	Asp	Gln		
			580					585					590				
Ile	Gly	Lys	Pro	Tyr	Asn	Ser	Ser	Gly	Leu	Gly	Gly	Pro	Ser	Ile	Lys		
		595					600					605					
Asp	Lys	Tyr	Val	Thr	Ala	Leu	Tyr	Phe	Thr	Phe	Ser	Ser	Leu	Thr	Ser		
	610					615					620						
Val	Gly	Phe	Gly	Asn	Val	Ser	Pro	Asn	Thr	Asn	Ser	Glu	Lys	Ile	Phe		
625					630					635					640		
Ser	Ile	Cys	Val	Met	Leu	Ile	Gly	Ser	Leu	Met	Tyr	Ala	Ser	Ile	Phe		
				645					650					655			
Gly	Asn	Val	Ser	Ala	Ile	Ile	Gln	Arg	Leu	Tyr	Ser	Gly	Thr	Ala	Arg		
			660					665					670				
Tyr	His	Thr	Gln	Met	Leu	Arg	Val	Arg	Glu	Phe	Ile	Arg	Phe	His	Gln		
		675					680					685					

Ile 690	Pro	Asn	Pro	Leu	Arg	Gln 695	Arg	Leu	Glu	Glu	Tyr 700	Phe	Gln	His	Ala
Trp 705	Ser	Tyr	Thr	Asn	Gly 710	Ile	Asp	Met	Asn	Ala 715	Val	Leu	Lys	Gly	Phe 720
Pro	Glu	Cys	Leu	Gln 725	Ala	Asp	Ile	Cys	Leu 730	His	Leu	Asn	Arg	Ser 735	Leu
Leu	Gln	His	Cys 740	Lys	Pro	Phe	Arg	Gly 745	Ala	Thr	Lys	Gly	Cys 750	Leu	Arg
Ala	Leu	Ala 755	Met	Lys	Phe	Lys	Thr 760	Thr	His	Ala	Pro	Pro 765	Gly	Asp	Thr
Leu	Val 770	His	Ala	Gly	Asp	Leu 775	Leu	Thr	Ala	Leu	Tyr 780	Phe	Ile	Ser	Arg
Gly 785	Ser	Ile	Glu	Ile	Leu 790	Arg	Gly	Asp	Val	Val 795	Val	Ala	Ile	Leu	Gly 800
Lys	Asn	Asp	Ile	Phe 805	Gly	Glu	Pro	Leu	Asn 810	Leu	Tyr	Ala	Arg	Pro 815	Gly
Lys	Ser	Asn	Gly 820	Asp	Val	Arg	Ala	Leu 825	Thr	Tyr	Cys	Asp	Leu 830	His	Lys
Ile	His	Arg 835	Asp	Asp	Leu	Leu	Glu 840	Val	Leu	Asp	Met	Tyr 845	Pro	Glu	Phe
Ser	Asp 850	His	Phe	Trp	Ser	Ser 855	Leu	Glu	Ile	Thr	Phe 860	Asn	Leu	Arg	Asp
Thr 865	Asn	Met	Ile	Pro	Gly 870	Ser	Pro	Gly	Ser	Thr 875	Glu	Leu	Glu	Gly	Gly 880
Phe	Ser	Arg	Gln	Arg 885	Lys	Arg	Lys	Leu	Ser 890	Phe	Arg	Arg	Arg	Thr 895	Asp
Lys	Asp	Thr	Glu 900	Gln	Pro	Gly	Glu	Val 905	Ser	Ala	Leu	Gly	Pro 910	Gly	Arg
Ala	Gly	Ala 915	Gly	Pro	Ser	Ser	Arg 920	Gly	Arg	Pro	Gly	Gly 925	Pro	Trp	Gly
Glu	Ser 930	Pro	Ser	Ser	Gly	Pro 935	Ser	Ser	Pro	Glu	Ser 940	Ser	Glu	Asp	Glu

Gly Pro Gly Arg Ser Ser Ser Pro Leu Arg Leu Val Pro Phe Ser Ser  
 945 950 955 960

Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met Glu Asp  
 965 970 975

Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala Phe Ser  
 980 985 990

Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly Arg Gln  
 995 1000 1005

Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu Leu  
 1010 1015 1020

Asn Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp Val  
 1025 1030 1035

Glu Ser Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu Glu  
 1040 1045 1050

Thr Arg Leu Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu Gln  
 1055 1060 1065

Arg Gln Met Thr Leu Val Pro Pro Ala Tyr Ser Ala Val Thr Thr  
 1070 1075 1080

Pro Gly Pro Gly Pro Thr Ser Thr Ser Pro Leu Leu Pro Val Ser  
 1085 1090 1095

Pro Leu Pro Thr Leu Thr Leu Asp Ser Leu Ser Gln Val Ser Gln  
 1100 1105 1110

Phe Met Ala Cys Glu Glu Leu Pro Pro Gly Ala Pro Glu Leu Pro  
 1115 1120 1125

Gln Glu Gly Pro Thr Arg Arg Leu Ser Leu Pro Gly Gln Leu Gly  
 1130 1135 1140

Ala Leu Thr Ser Gln Pro Leu His Arg His Gly Ser Asp Pro Gly  
 1145 1150 1155

Ser

<210> 4  
 <211> 732  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(445)

<400> 4

caaatccaga aaagatccgt tttcctaacc ttgttcgcct attttattat ttaaattgca  
60

gcaggagggga agc atg tct act tta tcc aat ttc aca cag acg ctg gaa  
109

Met Ser Thr Leu Ser Asn Phe Thr Gln Thr Leu Glu

1

5

10

gac gtc ttc cga agg att ttt att act tat atg gac aat tgg cgc cag  
157

Asp Val Phe Arg Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln

15

20

25

aac aca aca gct gag caa gag gcc ctc caa gcc aaa gtt gat gct gag  
205

Asn Thr Thr Ala Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu

30

35

40

aac ttc tac tat gtc atc ctg tac ctc atg gtg atg att gga atg ttc  
253

Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe

45

50

55

60

tct ttc atc atc gtg gcc atc ctg gtg agc act gtg aaa tcc aag aga  
301

Ser Phe Ile Ile Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg

65

70

75

cgg gaa cac tcc aat gac ccc tac cac cag tac att gta gag gac tgg  
349

Arg Glu His Ser Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp

80

85

90

cag gaa aag tac aag agc caa atc ttg aat cta gaa gaa tcg aag gcc  
397

Gln Glu Lys Tyr Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala

95

100

105

acc atc cat gag aac att ggt gcg gct ggg ttc aaa atg tcc ccc tga  
445

Thr Ile His Glu Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro

110

115

120

taagggagaa aggcaccaag ctaacatctg acgtccagac atgaagagat gccagtgcca  
505

cgaggcaaat ccaaattgtc tttgcttaga agaaagtgag ttccttgctc tctgttgaga  
565

attttcatgg agattatgtg gttggccaat aaagatagat gacatttcaa tctcagtgat  
625

ttatgcttgc ttgttggagc aatattttgt gctgaagacc tcttttactt tccgggcaag  
685

tgaatgtcat tttaatcaat atcaatgatg aaaataaagc caaattt  
732

<210> 5

<211> 123

<212> PRT

<213> Homo sapiens

<400> 5

Met Ser Thr Leu Ser Asn Phe Thr Gln Thr Leu Glu Asp Val Phe Arg  
1 5 10 15

Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln Asn Thr Thr Ala  
20 25 30

Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu Asn Phe Tyr Tyr  
           35                          40                          45

Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ser Phe Ile Ile  
       50                          55                          60

Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser  
       65                          70                          75                          80

Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Glu Lys Tyr  
                           85                          90                          95

Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala Thr Ile His Glu  
                           100                          105                          110

Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro  
           115                          120

<210> 6  
 <211> 21  
 <212> DNA  
 <213> synthetic construct

<400> 6  
 tttcaaagat atgcaattct g  
       21

<210> 7  
 <211> 20  
 <212> DNA  
 <213> synthetic construct

<400> 7  
 aagtccattt ttacagttca  
       20